

SEQUENCE SUBMISSION

SEQ ID NO: 1 is mouse 499E9 nucleic acid sequence.

SEQ ID NO: 2 is mouse 499E9 amino acid sequence.

(1) GENERAL INFORMATION:

(i) APPLICANT: Gorman, Daniel M.
Mattson, Jeanine D.

(ii) TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related Reagents

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE: 12-DEC-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/032,846
(B) FILING DATE: 13-DEC-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.
(B) REGISTRATION NUMBER: 34,090
(C) REFERENCE/DOCKET NUMBER: DX0686

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650)852-9196
(B) TELEFAX: (650)496-1200

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

09671658-092700

(ii) MOLECULE TYPE: cDNA

5

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 125..1072

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCCAGGACCT CTGTGAACCG GTCGGGGCGG GGGCCGCCTG GCCGGGAGTC TGCTCGGCGG 60
 TGGGTGGCCG AGGAAGGGAG AGAACGATCG CGGAGCAGGG CGCCCGAACT CCGGGCGCCG 120
 15 CGCC ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG TAC CTG CGC AGC TCG 169
 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser
 1 5 10 15
 20 GAG GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC GAG GGT CCG CTG CAC 217
 Glu Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His
 20 25 30
 25 CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA CCC GCC GCC TCC CGC 265
 Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg
 35 40 45
 30 TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG GGC CAG GTG GTC TGC 313
 Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys
 50 55 60
 35 AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG ATG GAT CCT AAC AGA 361
 Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg
 65 70 75
 40 ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA ATC CTG AGA CTC CAT 409
 Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His
 80 85 90 95
 45 GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG AGT GAA GAC ACA CTA 457
 Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu
 100 105 110
 50 CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT CAG GGG GCC GTG CAG 505
 Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln
 115 120 125
 55 AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC TTC TCA GGA GCT CCA 553
 Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro
 130 135 140
 60 GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC CAG CGA GGC AAG CCT 601
 Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro
 145 150 155

55

002260-092700

	GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT GCT GCC AGC ATC CCA Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro 160 165 170 175	649
5	TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG TAC CAC GAT CGA GGC Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly 180 185 190	697
10	TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC GGA AAA CTA AGG GTT Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val 195 200 205	745
15	AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC ATT TGC TTT CGG CAT Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His 210 215 220	793
20	CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT CTT CAG CTG ATG GTG His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val 225 230 235	841
	TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT AAC CTG ATG Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met 240 245 250 255	889
25	AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT TCT GAA TTC CAC TTT Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe 260 265 270	937
30	TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC CGA GCT GGT GAA GAA Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu 275 280 285	985
35	ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG GAT CCG GAT CAA GAT Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp 290 295 300	1033
40	GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC ATA GAC TGAGACTCAT Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp 305 310 315	1082
	TTCGTGGAAC ATTAGCATGG ATGTCCTAGA TGT TTGGAAA CTTCTTAAAA AATGGATGAT	1142
	GTCTATACAT GTGTAAGACT ACTAAGAGAC ATGGCCCACG GTGTATGAAA CTCACAGCCC	1202
45	TCTCTCTTGA GCCTGTACAG GTTGTGTATA TGTAAAGTCC ATAGGTGATG TTAGATTTCAT	1262
	GGTGATTACA CAACGGTTTT ACAATTTTGT AATGATTTCC TAAGAATTGA ACCAGATTGG	1322
50	GAGAGGTATT CCGATGCTTA TGAAAACTT ACACGTGAGC TATGGAAGGG GGTCACAGTC	1382
	TCTGGGTCTA ACCCCTGGAC ATGTGCCACT GAGAACCTTG AAATTAAGAA GATGCCATGT	1442
	CATTGCAAAG AAATGATAGT GTGAAGGGTT AAGTTCTTTT GAATTGTTAC ATTGCGCTGG	1502
55	GACCTGCAAA TAAGTTCTTT TTTTCTAATG AGGAGAGAAA AATATATGTA TTTTATATA	1562

002260 85942960

5 ATGTCTAAAG TTATATTTCA GGTGTAATGT TTTCTGTGCA AAGTTTTGTA AATTATATTT 1622
 GTGCTATAGT ATTTGATTCA AAATATTTAA AAATGTCTCA CTGTTGACAT ATTTAATGTT 1682
 TTAAATGTAC AGATGTATTT AACTGGTGCA CTTTGTAAAT CCCCTGAAGG TACTCGTAGC 1742
 TAAGGGGGCA GAATACTGTT TCTGGTGACC ACATGTAGTT TATTTCTTTA TTCTTTTTAA 1802
 10 CTTAATAGAG TCTTCAGACT TGTCAAAAC ATGCAAGCAA AATAAATAA TAAAAATAA 1862
 ATGAATATCT TGAATAATA GTAGGATGTT GGTCAACAGG TGCCTTTCAA ATTTAGAAGC 1922
 TAATTGACTT TAGGAGCTGA CATAGCCAAA AAGGATACAT AATAGGCTAC TGAAAATCTG 1982
 15 TCAGGAGTAT TTATGCAATT ATTGAACAGG TGTCTTTTTT TACAAGAGCT ACAAATTGTA 2042
 AATTTTGTTC CTTTTTTTTC CCATAGAAAA TGTACTATAG TTTATCAGCC AAAAAACAAT 2102
 20 CCACTTTTTC ATTTAGTGAA AGTTATTTTC TTATACTGTA CAATAAAGC ATTTGTTTCTG 2162
 AATGGCATT TTTGGTACTT AAAAATGGC 2191

25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

35 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
 1 5 10 15
 40 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
 20 25 30
 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Ala Ala Ser Arg Ser
 35 40 45
 45 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50 55 60
 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65 70 75 80
 50 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
 85 90 95
 55 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
 100 105 110

002250" 859T 2960

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
 115 120 125
 5 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
 130 135 140
 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
 145 150 155 160
 10 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
 165 170 175
 Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
 15 180 185 190
 Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
 195 200 205
 20 Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
 210 215 220
 Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
 225 230 235 240
 25 Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
 245 250 255
 Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
 260 265 270
 30 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
 275 280 285
 35 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
 290 295 300
 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 305 310 315
 40

002250"85912950